AMENDMENTS TO THE CLAIMS

1-6. (Canceled).

7. (Currently Amended) A method for producing a genomic DNA library, comprising the steps of

(1) preparing a mixture of fragmented DNAs having distribution ratio of 1 to 5 as defined by the size ratio (distribution ratio) of the maximum size of fragmented DNA to the minimum size of fragmented DNA and having a size convergence rate of 80% or more, wherein said mixture of fragmented DNAs is prepared by hydrodynamic point-sink shearing method, and wherein said mixture of fragmented DNAs is a mixture of DNAs having an average size of from 0.5 kbp to 2.5 kbp; and

(2) subjecting the mixture of fragmented DNAs obtained in step (1) to nucleic acid amplification using amplification primers, thereby producing DNAs corresponding to said mixture of fragmented DNAs, to give a genomic DNA library maintaining 85% or more of copy numbers of a set of genes or sequences on a genomic DNA and an abundance ratio of said set of genes or sequences on the genomic DNA.

8-12. (Canceled).

13. (Currently Amended) A method for producing a genomic DNA library, comprising the steps of:

(a) preparing a mixture of fragmented DNAs having distribution ratio of 1 to 5 as defined

by the size ratio (distribution ratio) of the maximum size of fragmented DNA to the minimum size of fragmented DNA and having a size convergence rate of 80% or more, wherein said mixture of fragmented DNAs is prepared by hydrodynamic point-sink shearing method, and wherein said mixture of fragmented DNAs is a mixture of DNAs having an average size of from 0.5 kbp to 2.5 kbp;

(b) ligating adapter DNA to the fragmented DNAs obtained in step (a), thereby giving DNA fragments; and

(c) ~~carrying out~~ subjecting the DNA fragments obtained in step (b) to nucleic acid amplification using ~~the DNA fragments obtained in step (b) as a template and~~ amplification primers, thereby producing DNAs corresponding to said mixture of fragmented DNAs, to give a genomic DNA library maintaining 85% or more of copy numbers of a set of genes or sequences on a genomic DNA and an abundance ratio of said set of genes or sequences on the genomic DNA.

14. (Cancelled).

15. (Original) The method according to claim 13, wherein said nucleic acid amplification in step (c) is Polymerase Chain Reaction (PCR) method.

16. (Original) The method according to claim 13, wherein said amplification primers used in the nucleic acid amplification in step (c) are primers selected from the group consisting of:

(i) oligonucleotides having a sequence complementary to said adapter DNA, and

(ii) oligonucleotides further comprising recognition sequences for restriction endonucleases, linker sequences and promoter sequence for RNA polymerase, in the sequence of the oligonucleotides of the above item (i).

17. (Original) The method according to claim 13, wherein the nucleic acid amplification in step (c) is carried out by using a DNA polymerase having a proofreading activity.

18. (Original) The method according to claim 17, wherein said DNA polymerase is a thermostable DNA polymerase.

19. (Original) The method according to claim 17, wherein said DNA polymerase is a mixture of a DNA polymerase having 3'→5' exonuclease activity and a DNA polymerase having no 3'→5' exonuclease activity.

20. (Original) The method according to claim 17, wherein said DNA polymerase is a mixture of at least two kinds of DNA polymerases, each having 3'→5' exonuclease activity.

21. (Original) The method according to claim 17, wherein said DNA polymerase is a mixture of α type DNA polymerase and non-α, non-pol I type DNA polymerase.

22-23. (Canceled).